

Figure 1

IM2169

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M978

10 20 30 40 50 60  
 CLGGGGSF DLD SVDT EAPR PAP KYQD VSSE K PQAQ K DQGGYGFAM RLK RRN WY PGAE -- ESEV KLN ESDW  
 =====  
 CLGGGGT F DLD SVDT EAPR PAP KYQD VSSE K PQAQ K DQGGYGFAM RLK RRN WHPQ ANPK EDEIKL SENDW  
 10 20 30 40 50 60 70  
  
 70 80 90 100 110 120 130  
 EATGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLT PNSHQN GSA GNGVNQPKNQATGHENFQYVYSG  
 =====  
 EATGLPGNPKNLPERQKSVIEKVKTGSDSNIYSSPYLT QSNHQN GSA -N-- QPKNEVKDYKEFKYVYSG  
 80 90 100 110 120 130  
  
 150 160 170 180 190 200  
 WFYKHAASE -- KDFS -NKKIKSGDDGYI FYHGEKPSRQLPASGKVI YKG VWHF VDT KKGQDFREIIQPS  
 =====  
 WFYKHALEI I KENN LIKG AKSGDDGYI FYHGEKPSRQLPVS GEV TYKG VWHF VDT KQGQKFNDILGTS  
 140 150 160 170 180 190 200  
  
 210 220 230 240 250 260 270  
 KKQGDRYSGFSGDGSEEYSNKNESTLKKDDHEGYGFTSNLEVDFGNKLTGKLIRNNASLNNTNNNDKHTT  
 =====  
 KKQGDRYSGFPGDDGEEYSNKNEATLQGSQEGYGFTSNLKVDFNKKLTGELIRNN -RVTNATANDKYTT  
 210 220 230 240 250 260 270  
  
 280 290 300 310 320 330 340  
 QYYSLDAQITGNRFNGTATATDKKEN -ETKLH P FVSDSSLSGGFFGPQGEELGFRFLSDDQKVAVVGSA  
 =====  
 QYYSLAQVTGNRFNGKATATDKPGTGETKQH P FVSDSSLSGGFFGPKGEELGFRFLSNDQKVAVVGSA  
 280 290 300 310 320 330 340  
  
 350 360 370 380 390 400 410  
 KTKDKLENG -- AAASGSTGAAASGGAAGTSSENS KLT TVLDAVELT LNDKKIKNLDFNSNAAQLVVDGIM  
 =====  
 KTQDKAANGNTAAASGGTDAASNGAAGTSSENS KLT TVLDAVELT LNDKKIKNLDFNSNAAQLVVDGIM  
 350 360 370 380 390 400 410  
  
 420 430 440 450 460 470  
 IPLL PKDSESGNTQADKGK -- NG -- G -TEFTRKFEHTPESDKD -- AQAGTQ -TNGAQTASNTAGDTNG  
 =====  
 IPLL PETSESGSNQADKGKKGKNGKNGGTDFTYKTTYTPKNDKD TKAQTGAAGSSGAQTDLGKADVN G  
 420 430 440 450 460 470 480  
  
 480 490 500 510 520 530 540  
 K -- TKT YEV EVC CSN LNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQN  
 =====  
 KAETKT YEV EVC CSN LNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQN  
 490 500 510 520 530 540 550

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550 560 570 580 590 600 610  
VVYRGSWYGHIA NGTWSGNASDKEGGNR A EFTVN FADKKITGKLTAENRQA QTFTI EGM IQGNGFEGTA  
===== ===== ===== ===== ===== ===== =====

560 570 580 590 600 610 620  
VVYRGSWYGHIA SSTS WSGN ASNATSGN RAEFTVN FDTK KINGTLTAENRQEATFTIDGKIEGN GFSGTA

620 630 640 650 660 670 680  
KTAESGFDL DQKNTTRTPKAYITDAKVQGGFYGPKAEEELGGWFAYPGDKQTEKATATSSDGN SASSATVV  
===== ===== ===== ===== ===== ===== =====

KTADLGFDL DQSNTT GTPKAYITDAKVQGGFYGPKAEEELGGWFAYPGDKQTEKATVASGDGN SASSATVV

630 640 650 660 670 680 690

690  
FGAKRQQPVQ  
=====

FGAKRQQPVQ  
700

Figure 2

IM2169

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6940

10 20 30 40 50 60 70  
 CLGGGGSFDLDSVDTEAPRPAPKYQDVSEKPOAQKDGQGYGFAMRLKRRNWYPGAEESEVKLNESDWEA  
 =====  
 CLGGGGTFDLDSVDTEAPRPDPKYQDVSEKPOAQKDGQGYGFAMRLKRRNWYSAAKEDEVKLNEDWET  
 10 20 30 40 50 60 70  
 80 90 100 110 120 130  
 TGLPTKPKELPKRQKSIEKVETD-GDSDIYSSPYLTPSNHONGSAGNGVNQPKNQATGHENFQYVYSGW  
 =====  
 TGLPTEPKKLPLKQESVISKVQANNGDNNIYTSPYLTQSNHQNSSINGGANLPKNEVTNYKDFKYVYSGW  
 80 90 100 110 120 130 140  
 150 160 170 180 190 200  
 FYKHAASE--KDFSNKK-IKSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKQDFREIIQPSK  
 =====  
 FYKHAKEIIIRENSSIKGAKNGDDGYIFYHGEKPSRQLPASGTVTYKGVWHFATDVKSQNFRDIIQPSK  
 150 160 170 180 190 200 210  
 210 220 230 240 250 260 270  
 KQGDRYSGFSGDGSEEYSNKNESTLKDDEGYGFTSNLEVDFGNKKLTGKLIRNNASLNNNTNNNDKHTTQ  
 =====  
 KQGDRYSGFSGDDDEQYSNKNEMLKDQEGYGFNTSNLEVDFGSKKLTGKLIRNN-RVTNAPTNDDKYTTQ  
 220 230 240 250 260 270  
 280 290 300 310 320 330 340  
 YYSLDAQITGNRFNGTATATDKKENE-TKLHPFVSDSSLSGGFFGPQGEELGFRFLSDDQKVAVVGSAK  
 =====  
 YYSLDAQITGNRFNGKAIRTDKPDGGTKLHPFVSDSSLSGGFFGPQGEELGFRFLSDDKKVAVVGSAK  
 290 300 310 320 330 340  
 350 360 370 380 390 400 410  
 TKDKLENGAAASGSTGAAASGGAAGTSSENKLTTVLDLAVELTLNDDKKNLNDNFNSAAQLVVDGIMIPL  
 =====  
 TKDKTENGAVASGGTDAAASNGAAGTSSENKLTTVLDLAVEKLGDKEVQKLDNFNSAAQLVVDGIMIPL  
 360 370 380 390 400 410  
 420 430 440 450 460 470 480  
 LPKDSESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQTNQATASNTAGDTNGKTKTYEVEVCCS  
 =====  
 LPEASESGNNQANQGTNGTAFTRKFDTPESDKKDAQAGTQTNQATASNTAGDTNGKTKTYEVEVCCS  
 430 440 450 460 470 480  
 490 500 510 520 530 540 550  
 NLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQNVVYRGSWYGHIA  
 =====  
 NLNYLKYGMLTRKNSKSAMQAGESSSQADAKTEQVEQSMFLQGERTDEKEIPSEQNIVYRGSWYGYIAND  
 500 510 520 530 540 550  
 560 570 580 590 600 610 620  
 --TSWSGNASDKEGGNRAEFTVNFADEKKITGKLTAENRQAQFTIEGMIQGNGFEGTAKTAESGF DLDQK  
 =====  
 KSTSWSGNASNATSGNRAEFTVNFADEKKITGTITADNRQEATFTIDGNIKDNGFEGTAKTAESGF DLDQK  
 570 580 590 600 610 620

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630 640 650 660 670 680 690  
NTTRTPKAYITDAVKGGFYGPKAELGGWFAYPGDKQT-EKATATSSDGNASSATVVFGAKRQQPVQ  
===== ===== = == - =====  
NTTRTPKAYITDAVKQGGFYGPKAELGGWFAYPGDKQT-KN-ATNASGNS-S-ATVVFGAKRQQPVR  
640 650 660 670 680 690

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Figure 3

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S3032

10	20	30	40	50	60	
CLGGGG-SFDLDSVDTEAPRPAKYQDVSSKEPKQAQKDQGGYGFAMRLKRRNWYPGAEESEVKLNESDWE						
10	20	30	40	50	60	70
CLGGGGGSFDLDSVDTEAPRPAKYQDVSSKEPKQAQKDQGGYGFAMRLKRRNWYPASKENEVKLNESDWE						
80	90	100	110	120	130	
ATGLPTPKELPKRQKSVIEKVETDGDSD--IYSSPYLTPSNHQNGSAGNGVNQPKNQATGHENFOYVY						
80	90	100	110	120	130	140
TTGLPSNPKNLPERQKSVIDQVETDGDSSNNSNIYSSPYLTQSNHQNGNTGNGVNQPKNEVTDYKNFKVYV						
140	150	160	170	180	190	200
SGWFYKHAASEKDFS-NKKI-KSGDDGYIFYHGEKPSRQLPASGKVIYGVWHFVTDTKKGQDFREIIQP						
150	160	170	180	190	200	210
SGWFYKHAKREVNLAPEPKIAKNGDDGYIFYHGDPSRQLPASGKITYGVWHFATDTKRGQKFREIIQP						
210	220	230	240	250	260	270
SKKQGDRYSGFSGDGSEEYSNKNESTLKDDEGYGFTSNLEVDGKLNKLTGKLIRNNASLNNNTNNDKHT						
220	230	240	250	260	270	280
SKNQGDRYSGFSGDDDEQYSNKNESMLKDGHEGYGFASNLEVDFDNKLNKLTGKLIRNNANQNNNTNNDKHT						
280	290	300	310	320	330	340
TQYYSLDAQITGNRFNGTATATDK-KEN-ETKLHPPVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVG						
290	300	310	320	330	340	350
TQYYSLDATLKGNRFSGKAEATDKPKNDGETKEHPPVSDSSSLSGGFFGPQGEELGFRFLSNDQKVAVVG						
350	360	370	380	390	400	410
SAKTKDKLENG-AA-ASGSTGAAASGGAAGTSSSENSKLTTVLDLDAVELTLNDKKIKNLDNFNSNAAQLVVDG						
360	370	380	390	400	410	420
SAKTKDKPANGNTAEASGGTAAASGGAAGTSSSENSKLTTVLDLDAVELTHGGTAIKNLDNFNSNAAQLVVDG						
420	430	440	450	460	470	480
IMIPLLKDSESGNTQADKGKNGGTEFTRKFENTPESDKDAQAGTQNTNGAQTASNTAGDTNGKTKTYEV						
430	440	450	460	470	480	490
IMIPLLQNSTGKNNQPDQGKNGGTAFIYKTTYTPKNDDKDTKAQTVTGGTQTAASNTAGDANGKTKTYEV						
490	500	510	520	530	540	550
EVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQNVVYRGSWYG						
500	510	520	530	540	550	
EVCCSNLNYLKYGMLTRKTAGNTVSGGNSSPTAAQTDAAQSMFLQGERTDENKIPSEQNVVYRGSWYG						
560	570	580	590	600	610	620
HIANGTWSGNASDKEGGNRAEFTVNFADKKITGKLTAENRQAQFTIEGMIQGNGFECTAKTAESGFDL						
570	580	590	600	610	620	
HIAASSTWSGNASDKEGGNRAEFTVNFGEKKITGTLTAENRQEATFTIDGKIEGNGFSGTAKTAELGFDL						

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630 640 650 660 670 680 690  
DQKNTTRTPKAYITDAVKGGFYGPKAEEELGGWFAYPGDKQTEKATATSSDGNASSATVVFGAKRQQPVQ  
===== ===== ===== ===== ===== =====  
DQKNTTRTPKAYITDAVKGGFYGPKAEEELGGWFAYSDDKQTKNATDASGNNSASSATVVFGAKRQQPVQ  
640 650 660 670 680 690

Figure 4

	10	20	30	40	50	60	
346	361	380					
1	TKDKLENGAA--ASGSGTAAASGGAAAGTSSSENSKLTTVLDAAVELTLNDKKIKNLDNFSNA						58
2	TKDKTENGAV--ASGGTDAAASNGAAGTSSSENSKLTTVLDAAVELKLGDKEVQKLDNFSNA						58
3	TKDKTENGAV--ASGGTDAAASNGAAGTSSSENSKLTTVLDAAVELKLGDKEVQKLDNFSNA						58
4	TQDKPRNGAV--ASGGTGAARSNGAAGQSSSENSKLTTVLDAAVELTLNDKKIKNLDNFSNA						58
5	TQDKAANGNTAAASGGTDAAASNGAAGTSSSENSKLTTVLDAAVELTLNDKKIKNLDNFSNA						60
6	KRDKAESGGNGASGGTDAAASNGAAGTSSSENSKLTTVLDAAVELKSGGKEVKNLDNFSNA						60
7	TKDKPRNGAV--ASGGTDAAASNGAAGTSSSENGKLTTVLDAAVELTLNDKKIKNLDNFSNA						58
8	TKDKPANGNTAEASGGTDAAASGGAAGTSSSENSKLTTVLDAAVELTHGGTAIKNLDNFSNA						60
9	TKDKPGNGA---RLQAARCGTSNGAAGQSSSENSKLTTVLDAAVELKLGDKEVQKLDNFSNA						57
C	*+DK: : *G+: : *+*****+**+5+GAAG+SSEN*KLTTVLDAAVEL: +: *: : +LDNFSNA						
	70	80	90	100	110	120	
	417			445			
1	AQLVVDGIMIPLLKDSESGNTQADKGK-----NGGTEFTRKFETHTPESDKDQAQAGTQ						112
2	AQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFDTHTPESDKDQAQAGTQ						112
3	AQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFDTHTPESDKDQAQAGTQ						112
4	AQLVVDGIMIPLLPEASESGKNOANQGT-----NGGTAFTRKFETTPKSDEKDQTQAGTA						112
5	AQLVVDGIMIPLLKDSESGNTQADKGK-----NGGTRKFTRKFETTPKSDEKDQTQAGTQ						120
6	AQLVVDGIMIPLLKDSESGNTQADKGK-----NGGTRKFTRKFETTPKSDEKDQTQAGTQ						114
7	AQLVVGIMIPLMPETSESGNNQADKGK-----NGGTAFTRKFETTPKSDEKDQTQAGTP						112
8	AQLVVDGIMIPLLKDSESGNNQADKGK-----NGGTAFTRKFETTPKSDEKDQTQAGTP						114
9	AQLVVDGIMIPLLKDSESGKNOADKGK-----NGETEFTRKFETHTPESDEKDQAQAGTP						111
C	AQLVVGIMIPLP: .S***+*Q*: :G: NG*T: F*+K+.+TP: +D: KD: +A+T:						
	130	140	150	160	170	180	
	465	482	499				
1	TNGAQTASNTAGDTNGKT-----RTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQ						167
2	TNGAQTASNTAGDTNGKT-----RTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSSQ						167
3	ANGAQTASNTAGDTNGKT-----RTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSSQ						167
4	ENGNPAASNTAGDANGKT-----RTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSSQ						167
5	AAGSSGAQTDLGKADVNGGKAETRTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQ						180
6	TNGAQTASNTAGDTNGKT-----RTYEVEVCCSNLNYLKYGLLTRKTAGNTGEGGNGSQT						169
7	TNGAQTASGTAGVTGGQAG---RTYAVEVCCSNLNYLKYGLLTRKTAGNTVCGNGSST						168
8	TGGTQTASNTAGDANGKT-----RTYEVEVCCSNLNYLKYGLLTRKTAGNTVCGNGSPT						169
9	SNGAQTASNTAGDTNGKT-----RTYEVNLC-SNLNYLKYGLLTRKTAGNTGEGGNGSPT						165
C	: +G+++A***+*G++**+. RTY*V**C*SNLNYLKYG: LTRK: : : : : : G: : S+: :						
	190	200	210				
	521						
1	ADAKTEQVEQSMFLQGERTDEKEIPTDQ-NVV						198
2	ADAKTEQVEQSMFLQGERTDEKEIPSEQ-NIV						198
3	ADAKTEQVQGQSMFLQGERTDEKEIPSEQ-NIV						198
4	ADAKTEQVQGQSMFLQGERTDEKEIPNDQ-NVV						198
5	ADAKTEQVEQSMFLQGERTDEKEIPNDQ-NVV						211
6	AAAQTAQGAQSMFLQGERTDEKEIPSEQ-NVV						200
7	AAAQTAQGAQSMFLQGERTDEKEIPKEQQDIV						200
8	AAAQTD--AQSMFLQGERTDENKIPSEQ-NVV						198
9	AA-QTAQGAQSMFLQGERTDEKEIPNDQ-NVV						195
C	A: *: T: *: :QSMFLQGERTDE**IP: :Q * +V						

Figure 5

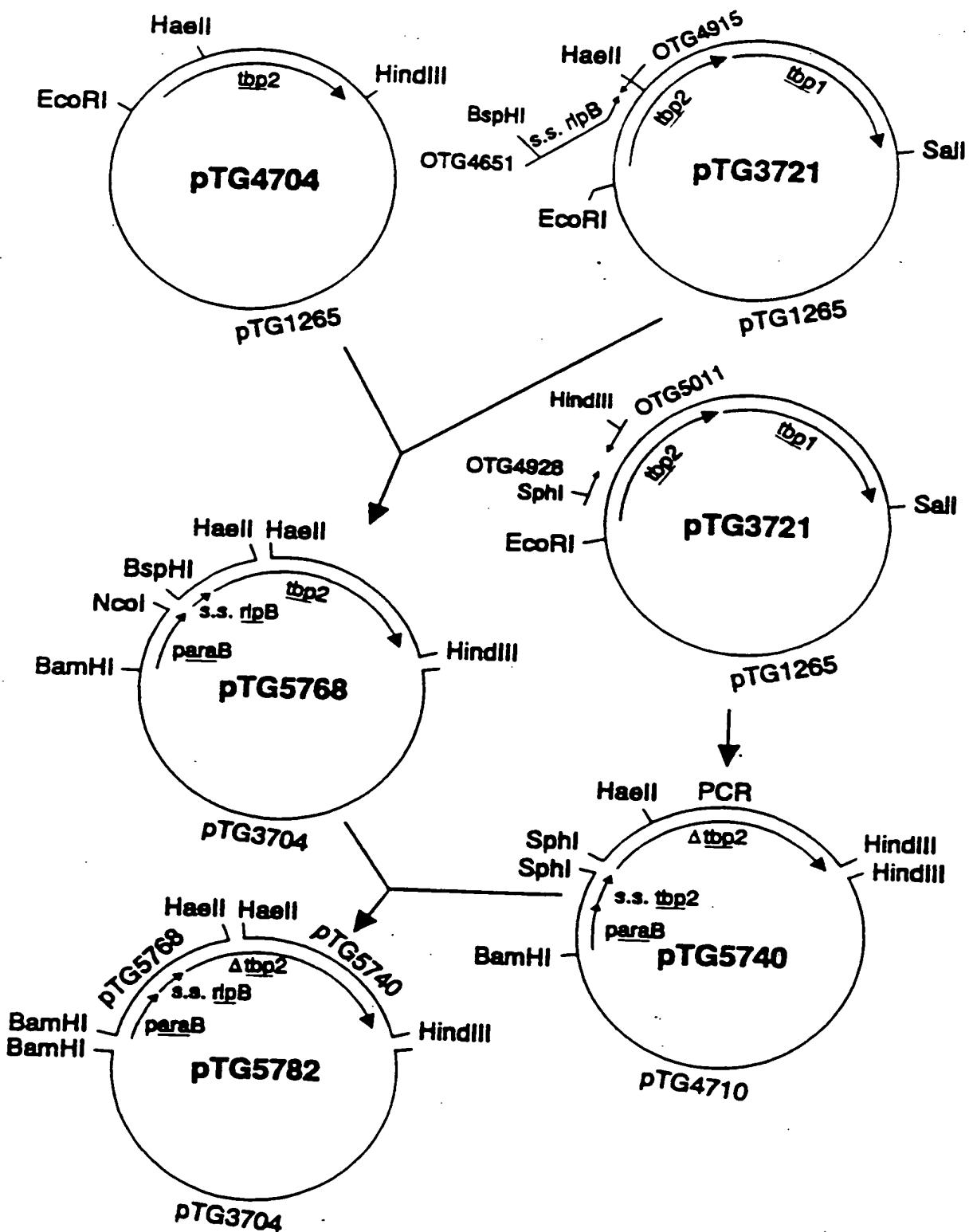


Figure 6

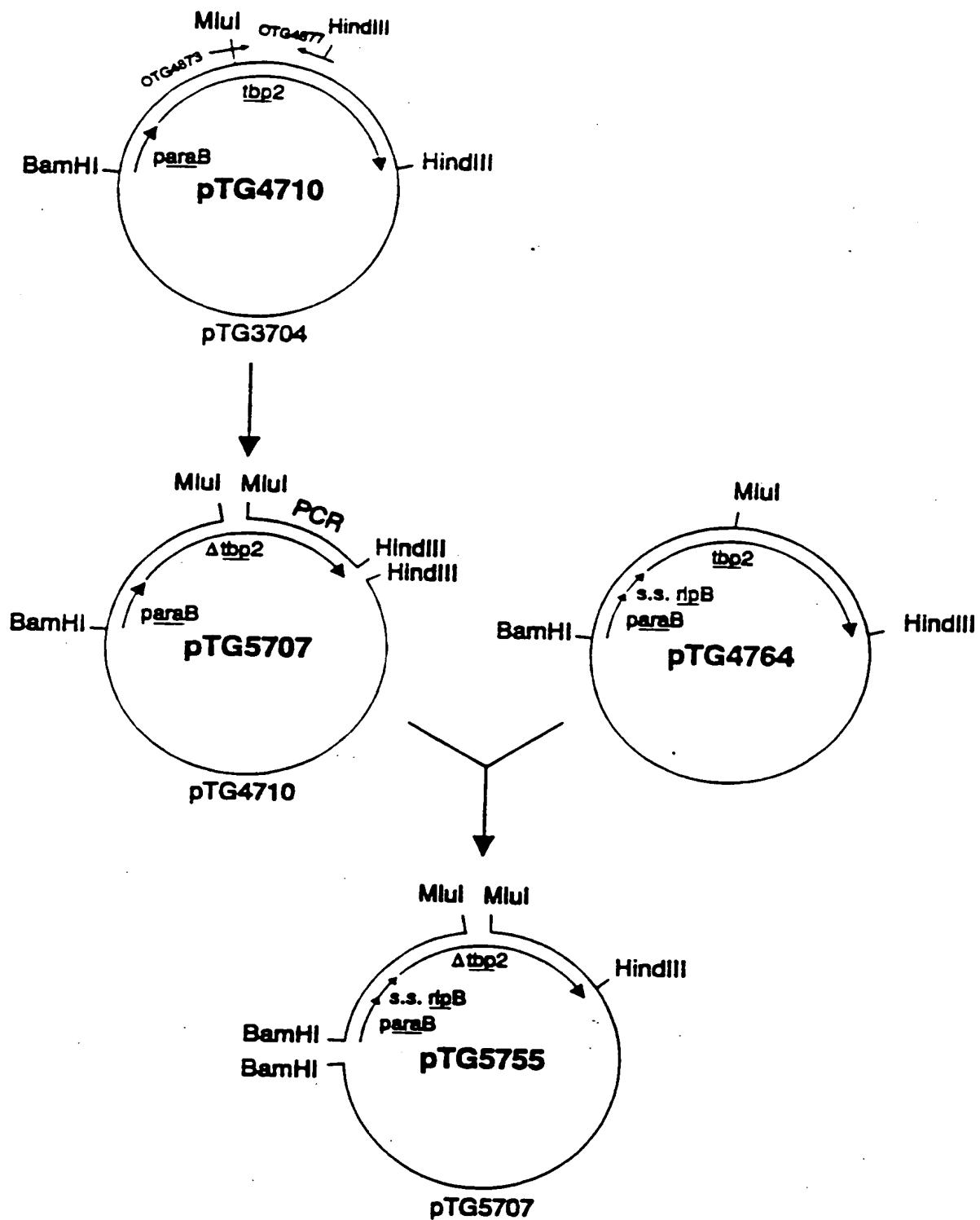
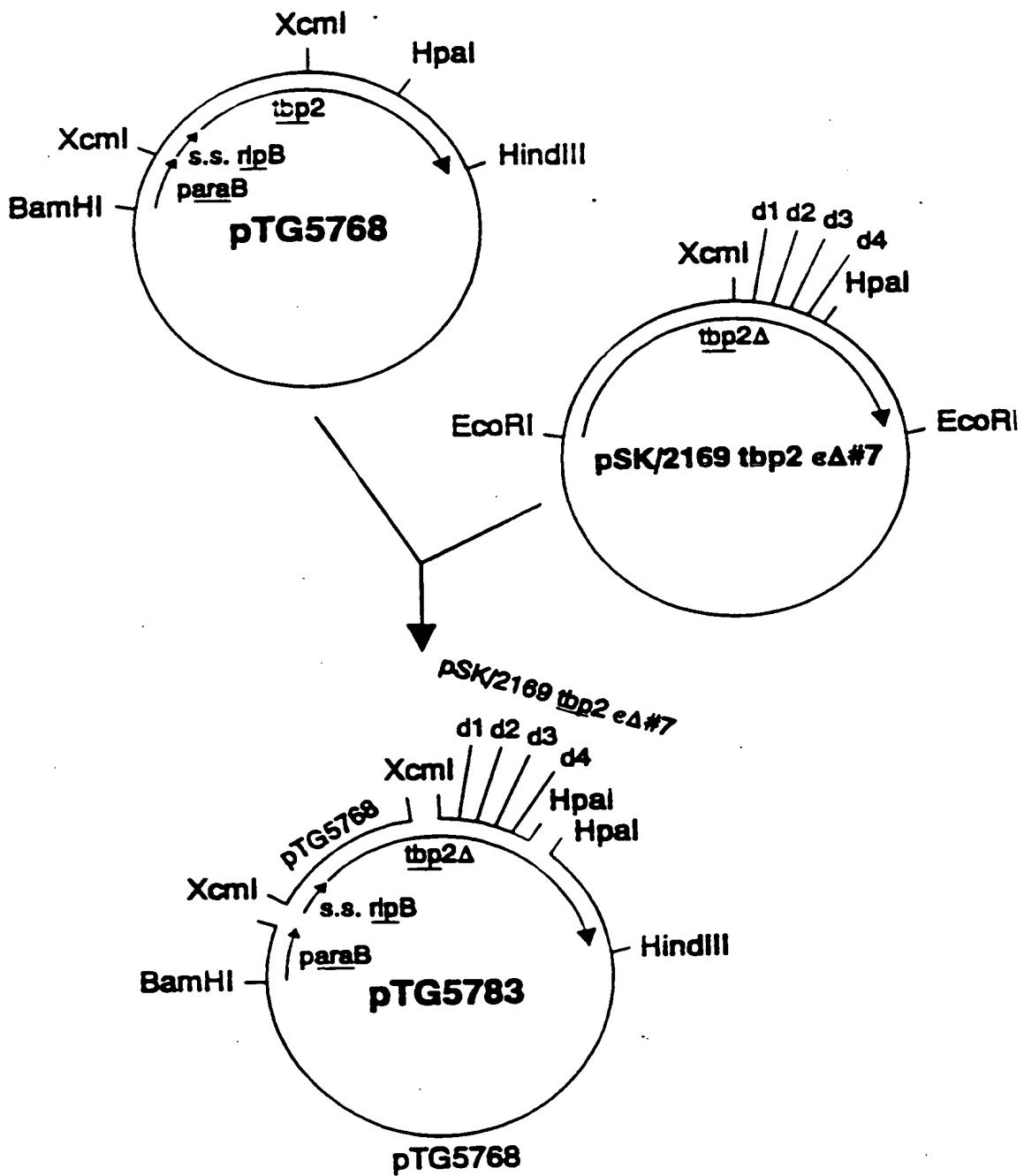


Figure 7



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PCT/P95/00701

WO 95/33049

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Figure 8

M982

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B283

10 20 30 40 50 60 70  
CLGGGGSFDLDSVDTEAPRPAKYQDVSEKPAQAKDQGGYGFAMRLKRRNWYPGAEESEVKLNESDWEA  
CLGGGGSFDLDSVDTEAPRPAKYQDVSETPQAQAKDQGGYGFAMRFKRRNWYPKNEEDHKALSEADWEK  
10 20 30 40 50 60 70  
80 90 100 110 120 130 140  
TGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTPSNHQNGSAGNGVNQPKNQATGHENFQYVYSGWF  
LG AGKPDEFPQRNE ILN M TDG ILSES L QL GE G G KSRVEGYTDFQYVRSGYI  
80 90 100 110 120 130 140  
150 160 170 180 190 200 210  
YKHAASEKDFSNKKIKSGDDGYIFYHGEKPSRQLPASGKVIYKGWVHFVTDKKGQDFREIIQPSKKQGD  
YRNGANKIDFQKKIALSGPDGYLFYKGNSNPSQALPM GKVGYKGTWDYVTDAKGQKFSQL AGFPAGD  
130 140 150 160 170 180  
220 230 240 250 260 270 280  
RYSGFSGDGSEEYSNKNESTLKDDEGYGFTSNLEVDFGNKKLTGKLIRNNASLNNTNNDKHTTQYYSL  
RYGALSAEEADVLRNKSEA QQGQTDGLTSEFEVDFAAKMTGALYRNNRITNNETENKAKQIKRYDI  
200 210 220 230 240 250  
290 300 310 320 330 340  
DAQITGNRFNGTATATDK KENETKLHPFVSDSSLSGGFFGPOGEELGFRFLSDDQKVAVVGSAKTKDK  
QADLHGNRFSGKATATDKPKNDTKEHPFVSDSSLSGGFFGPKGEELGFRFLSDDQKVAVVGSAKTKDK  
260 270 280 290 300 310 320  
360 370 380 390 400 410  
LENGAAASGSTGAAASGGAAGTSSENSKLTTVLDLDAVELTLNDKKIKNLDNFNSAAQLVVDGIMIPLLKD  
LENGAAASGSTGAAASGGAADMPSENGKLTTVLDLDAVELKSGGKEVKNLDNFNSAAQLVVDGIMIPLLKD  
330 340 350 360 370 380 390  
430 440 450 460 470 480  
SESGNTQADKGKNGGTEFTRKFEHTPESDKDAQAGTQNTGAQTAQNTAGDTNGKTKTYEVEVCCSNLNY  
SESESNQADKGKNGGTAFTRKFEHTPESDKDTQAGTAENGNAQNTAGDTNGKTKTYEVEVCCSNLNY  
400 410 420 430 440 450 460  
500 510 520 530 540 550  
LKYGMLTRNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQ NVVYRGSWYGHIAINTSW  
LKYGMLTRNSKSAMQAGENGSLADAKTEQVEQSMFLQGERTDEKEIPKEQQDIVYRGSWYGHIAINTSW  
470 480 490 500 510 520 530  
570 580 590 600 610 620  
SGNASDKEGGNRAEFTVNFADKKITGKLTAEQRQAQFTIEGMIQGNGFEGTAKTAESGFDLQKNTTRT  
SGNASDREGGNRADFTVNFGTKKINGTLTAENRQEATFTIVGDIKDNGFEGTAKTADSGFDLQDQSNTTRT  
540 550 560 570 580 590 600

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640 650 660 670 680 690  
PKAYITDAVKGGFYGPKAEEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQQPVQ  
PKAYITDAVKGGFYGPKAEEELGGWFAYPGDKQTEKATVTSGDGLSASSATVVFGAKRQKPVQ  
610 620 630 640 650 660

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Figure 9

M982

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BZ163

10	20	30	40	50	60
CLGGGGSFDLDSVDTEAPRPAP KYQDVSSSEKPQAQKDQGGYGFAMRLKRRNWYPGAESEVKLNESDWE					
10	20	30	40	50	60
CLGGGGSFDLDSVDTEAPRPAPPKYQDVSSSEKPQAQKDQGGYGFAMRLKRRNRHPQAEDKVELNPNDWE					
10	20	30	40	50	60
80	90	100	110	120	130
ATGLPTPKELPKRQKSVIEKVETDGDSIYSSPYLTPSNHQNGSAGNGVNQPKNQATGHENFOYVYSGW					
80	90	100	110	120	130
ETGLPSKPQNLPERQQSVIDKVKTDDGSNIYTSPYLTQSNHQNGSTNSGANQPKNEVKDYKNFKYVYSGW					
80	90	100	110	120	130
150	160	170	180	190	200
FYKHAASEKDFSNKKIKSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSKKQG					
150	160	170	180	190	200
FYKHAESEREFSKIKFKSGDDGYIFYHGDPSRQLPTSEKVIYKGVWHFVTDTKEKGQKFNDILETSKGQG					
150	160	170	180	190	200
220	230	240	250	260	270
DRYSGFSGDGSEEYSNKNESTLKDDEGYGFTSNLEVDFGNKLTGKLIRNNASLNNNTNNDKHTTQYYS					
220	230	240	250	260	270
290	300	310	320	330	340
LDAQITGNRFNGTATADKKE NE TKLHPFVSDSSSLGGFFGPQGEELGFRFLSDDQKVAVVGSAKTKD					
290	300	310	320	330	340
360	370	380	390	400	410
KLENGAAASGSTGAAASGGAAGTSSSENSKLTTVLDARELTLNDKKIKNLDNFNSAAQLVVDGIMIPLLPK					
360	370	380	390	400	410
430	440	450	460	470	480
DSESGNTQADKGKNGTEFTRKFHPTPESDKDAQAGTQNTGAQTAQNTAGDTNGKTKTYEVEVCCSNLN					
430	440	450	460	470	480
500	510	520	530	540	550
YLYGMLTRKNSKSAMQAGGNSSQADAKTEQVQSMFLQGERTDEKEIPTDQNVVYRGSWYGHIASTSW					
500	510	520	530	540	550
570	580	590	600	610	620
SGNASDKEGGNRAEFTVNFAADKKITGKLTAEQRQAQFTIEGMIQGNGFEGTAKTAESGFDLQKNTTRT					
570	580	590	600	610	620

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640 650 660 670 680 690  
PKAYITDAVKGGFYGPKAELGGWFAYPGDKQTEKATATSSDGN  
SASSATVVFGAKRQQPVQ  
===== ===== ===== =- ===== ===== =====  
640 650 660 670 680 690  
PKAYITDAKVQGGFYGPKAELGGWFAYQGDKQTENTTVASGN  
GNSASSATVVFGAKRQKPVQ

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Figure 10

	10	20	30	40	50	60
346	361	380				
1	TKDKLENG--AAASGSTGAAASGGAAGTSENSKLTTVLDACHELTLNDDKKIKNLDNFSN					57
2	TKDKTENG--AVASGGTDAASNGAAGTSENSKLTTVLDACHELKLGDKEVQKLDNFSN					57
3	TQDKPRNG--AVASGGTGAARSNGAAGQSENSKLTTVLDACHELTLNDDKKIKNLDNFSN					57
4	TKDNTANGNTAAASGGTDAASNGAAGTSENGKLTTVLDACHELTLNDDKKIKNLDNFSN					60
5	TKDKTENG--AVASGGTDAASNGAAGTSENSKLTTVLDACHELKLGDKEVQKLDNFSN					57
6	TQDKAANGNTAAASGGTDAASNGAAGTSENSKLTTVLDACHELTLNDDKKIKNLDNFSN					59
7	RDKDAESGGGNGASGGTDAASNGAAGTSENGKLTTVLDACHELKSGGKEVKNLDNFSN					59
8	TKDKPANGNTAEASGGTDAASNGAAGTSENGKLTTVLDACHELTHGGTAIKNLDNFSN					59
9	TKDKPRNG--AVASGGTDAASNGAAGTSENGKLTTVLDACHELTLNDDKKIKNLDNFSN					57
10	TKDKLENG--AAASGSTGAAASGGAADMPSENGKLTTVLDACHELKSGGKEVKNLDNFSN					57
11	TKDKTENG--AVASGGTDAASNGAAGTSENGKLTTVLDACHELKLGDKEVQKLDNFSN					57
C	**D*.:*G..*:ASG*T+AA*S+GAA***SEN+KLTTVLDACHEL:+:+*:++LDNFSN					

	70	80	90	100	110	120
	417				445	
1	AAQLVVDGIMIPLLKDSESGNTQADKGK-----NGGTEFTRKFERTPESDKKDAQAGT					111
2	AAQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFERTPESDKKDAQAGT					111
3	AAQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFERTPKSDEKDTQAGT					111
4	AAQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFERTPKSDEKDTHAGT					114
5	AAQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFERTPKSDEKDTQAGT					111
6	AAQLVVDGIMIPLLPEASESGNSNQADKGKRGKRNQNGTDFTYKTTYTPKNDKDQAGT					119
7	AAQLVVDGIMIPLLKDSESGNTQADKGK-----NGGTFKTRKFERTPESDKKDAQAGT					113
8	AAQLVVDGIMIPLLQNSTGKNNQPDQGK-----NGGTAFTRKFERTPKNDDKDQAGT					113
9	AAQLVVGIMIPLMPETSESGNNQADKGK-----NGGTAFTRKFERTPKSDEKDTQAGT					111
10	AAQLVVDGIMIPLLPRNSESESNSNQADKGK-----NGGTAFTRKFERTPESDKKDTQAGT					111
11	AAQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTRKFERTPESDKKDAQAGT					111
C	AAQLVVGIMIPLMPETSESGNNQADKGK-----NGGTAFTRKFERTPKSDEKDTQAGT					

	130	140	150	160	170	180
	465	482	482	499		
1	QTNGAQTASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSS					166
2	QANGAQTASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSS					166
3	AENGNPAAASNTAGDANG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSS					166
4	AANGDQAASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSS					169
5	QTNGAQTASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSS					166
6	GAAGSSGAQTDLGKADVNGGKAETKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSS					179
7	QTNGAQTASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNTAGNTGEGGNSSQ					168
8	VTGGTQTAASNTAGDANG-----KTKTYEVEVCCSNLNYLKYGMLTRKNTAGNTVGSGNSSP					168
9	PTNGAQTASGTAGVTGGQAG-----KTYAVEVEVCCSNLNYLKYGMLTRKNTADNTVGSGNSS					167
10	AENGNPAAASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGENGSS					166
11	QTNGAQTASNTAGDTNG-----KTKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGESSS					166
C	**G:++A*****G+***+:KTY*VEVCCSNLNYLKYG+LTK++++++G:++					

Figure 10 (continuation)

	190	200	210	
521				
1	QADAKTEQVEQSMFLQGERTDEKEIPTDQ-NVV			198
2	QADAKTEQVGQSMFLQGERTDEKEIPSEQ-NIV			198
3	QADAKTEQVGQSMFLQGERTDEKEIPNDQ-NVV			198
4	TAAQTAQGAQSMFLQGERTDEKEIPSEQ-NV-			200
5	QADAKTEQVEQSMFLQGERTDEKEIPSEQ-NIV			198
6	QADAKTEQVEQSMFLQGERTDEKEIPNDQ-NV-			210
7	TAAQTAQGAQSMFLQGERTDEKEIPSEQ-NV-			199
8	TAAQTAQGAQSMFLQGERTDENKIPSEQ-NVV			198
9	TAAQTAQGAQSMFLQGERTDEKEIPKEQQDIV			200
10	LADAKTEQVEQSMFLQGERTDEKEIPKEQQDIV			199
11	QADAKTEQVGQSMFLQGERTDEKEIPSEQ-NIV			198
C	:A+A+T+*+.QSMFLQGERTDE**IP:+Q *:+			